

09/991433

L1 FILE 'REGISTRY' ENTERED AT 14:08:04 ON 20 JAN 2004
123 S NKGTTQYT | QQYTDQ/SQSP

L2 FILE 'HCAPLUS' ENTERED AT 14:10:10 ON 20 JAN 2004
15 S L1

L2 ANSWER 1 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:757225 HCAPLUS

DOCUMENT NUMBER: 139:272071

TITLE: Gene disruption method GRACE (gene replacement and conditional expression) for identification of drug targets in Candida albicans and other diploid fungal pathogens

INVENTOR(S): Roemer, Terry; Jiang, Bo; Boone, Charles; Bussey, Howard; Ohlsen, Kari L.

PATENT ASSIGNEE(S): Elitra Pharmaceuticals, Inc., USA

SOURCE: U.S. Pat. Appl. Publ., 79 pp., Cont.-in-part of U.S. Ser. No. 792,024.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003180953	A1	20030925	US 2001-32585	20011220
PRIORITY APPLN. INFO.:			US 2000-259128P	P 20001229
			US 2001-792024	A2 20010220
			US 2001-314050P	P 20010822

AB The present invention provides methods and compns. that enable the exptl. determination as to whether any gene in the genome of a diploid pathogenic organism is essential, and whether it is required for virulence or pathogenicity. The method designated GRACE (gene replacement and conditional expression) involve the construction of genetic mutants in which one allele of a specific gene is inactivated while the other allele of the gene is placed under conditional expression. The identification of essential genes and those genes critical to the development of virulent infections, provides a basis for the development of screens for new drugs against such pathogenic organisms. The present invention further provides 932 Candida albicans genes that are demonstrated to be essential and are potential targets for drug screening. The nucleotide sequence of the target genes can be used for various drug discovery purposes, such as expression of the recombinant protein, hybridization assay, and construction of nucleic acid arrays. The uses of proteins encoded by the essential genes, and genetically engineered cells comprising modified alleles of essential genes in various screening methods are also encompassed by the invention.

IT 604833-49-0

RL: AGR (Agricultural use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(amino acid sequence; GRACE (gene replacement and controlled expression) and use of gene disruption methods for identification of drug targets in diploid fungal pathogens)

L2 ANSWER 2 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:58723 HCAPLUS

09/991433

DOCUMENT NUMBER: 138:103553
TITLE: Use of B19 parvovirus VP2 capsid particles in the inhibition of hematopoietic origin or endothelial cell proliferation and migration
INVENTOR(S): Broliden, Kristina; Westgren, Magnus
PATENT ASSIGNEE(S): Swed.
SOURCE: U.S. Pat. Appl. Publ., 52 pp., Cont.-in-part of U.S. Ser. No. 447,693.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003017596	A1	20030123	US 2001-991433	20011116
SE 9804022	A	20000525	SE 1998-4022	19981124
SE 520177	C2	20030603		

PRIORITY APPLN. INFO.: SE 1998-4022 A 19981124
US 1999-447693 A2 19991123

AB The invention described herein relates to methods, compns. and sequences of parvovirus B19 fragments for the inhibition of growth and/or migration of cells that have a receptor that interacts with a parvovirus B19 capsid or fragment thereof (e.g., a P antigen containing cell), including but not limited to, cells of hematopoietic origin and endothelial cells. More specifically, parvovirus capsid particles or fragments of parvovirus capsid proteins are used to manufacture medicaments that can be administered to a subject to inhibit hematopoietic progenitor cell growth (e.g., prior to stem cell transplantation), endothelial cell growth, (e.g., as an anti-tumorigenesis treatment or to prevent restenosis or fibrotic build up following prosthetic implantation), or to prevent disorders that involve the abnormal proliferation of cells that have the P antigen (e.g., Polycythemia Vera).

IT 488728-15-0P 488728-16-1P 488728-17-2P
488728-60-5P

RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(parvovirus VP2 capsid protein fragment amino acid sequence; use of B19 parvovirus VP2 capsid particles in inhibition of hematopoietic origin or endothelial cell proliferation and migration)

IT 488728-12-7 488728-13-8 488728-14-9

RL: PRP (Properties)
(unclaimed sequence; use of B19 parvovirus VP2 capsid particles in the inhibition of hematopoietic origin or endothelial cell proliferation and migration)

L2 ANSWER 3 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2003:23044 HCAPLUS

DOCUMENT NUMBER: 138:84433

TITLE: Nucleic acid-based diagnostic assays for parvovirus B19

INVENTOR(S): Pichuantes, Sergio; Shyamala, Venkatakrishna

PATENT ASSIGNEE(S): Chiron Corporation, USA

SOURCE: PCT Int. Appl., 148 pp.

Searcher : Shears 571-272-2528

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CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003002753	A2	20030109	WO 2002-US20684	20020628
<p>W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM</p> <p>RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG</p>				
US 2003170612	A1	20030911	US 2002-187253	20020628
PRIORITY APPLN. INFO.:			US 2001-302077P	P 20010628
			US 2002-365956P	P 20020319
			US 2002-369224P	P 20020329
<p>AB The present invention is based on the discovery of unique primers and probes for use in nucleic acid-based assays, as well as on the development of a sensitive, reliable nucleic acid-based diagnostic test for the detection of parvovirus B19 DNA in biol. samples from potentially infected individuals. The techniques utilize extracted sample DNA as a template for amplification of conserved genomic regions of the B19 sequence using transcription-mediated amplification (TMA), as well as in a 5'-nuclease assay, such as the TaqMan® technique. The methods allow for the detection of B19 DNA in viremic samples having viral titers as low as 10³ virus particles/mL. Accordingly, infected samples can be identified and excluded from transfusion, as well as from the preparation of blood derivs. The probes and primers described are also useful in, for example, standard hybridization methods, as well as PCR-based techniques, nucleic acid sequence-based amplification (NASBA), and in assays that utilize branched DNA mols.</p>				
<p>IT 482672-19-5, Protein VP1 (B19 virus clone 2-B1) 482672-21-9, Protein VP2 (B19 virus clone 2-B1) 482672-25-3, Protein VP1 (B19 virus clone 2-B6) 482672-27-5, Protein VP2 (B19 virus clone 2-B6) RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (amino acid sequence; nucleic acid-based diagnostic assays for parvovirus B19)</p>				
<p>L2 ANSWER 4 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN ACCESSION NUMBER: 2002:851429 HCAPLUS DOCUMENT NUMBER: 138:164464 TITLE: A New Parvovirus Genotype Persistent in Human Skin AUTHOR(S): Hokynar, Kati; Soederlund-Venermo, Maria; Pesonen, Maria; Ranki, Annamari; Kiviluoto, Olli; Partio, Esa K.; Hedman, Klaus CORPORATE SOURCE: Department of Virology, University of Helsinki, Helsinki, FIN-00290, Finland</p>				

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SOURCE: Virology (2002), 302(2), 224-228
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Parvovirus B19 is the exclusive human pathogen of the Erythrovirus genus. In classical view, the B19 DNA sequence shows little variability, with no disease-specific or tissue type specific assocns. We examined skin biopsies from patients with B19-unrelated skin disease or from constitutionally healthy adults by polymerase chain reaction assays for four different genomic regions of the B19 virus. Sequencing showed that the skin-derived viral DNA differed within the protein-coding region from the B19 reference sequences by 10.8% and from the V9 variant by 8.6% and within the noncoding region (covering nucleotides 189-435 of the promoter region) by 26.5 and 17.2%, resp. Despite this sequence difference, the promoter region was shown by a luciferase gene expression assay to be biol. active. We have detected a new B19 virus genotype, K71, which differs extensively from the known B19-virus genotypes and is persistently carried in human skin.

IT 488188-04-1 488188-05-2 488188-07-4
488188-08-5

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; protein and DNA sequence of new parvovirus genotype K71 persistent in human skin)

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 5 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:728591 HCAPLUS
DOCUMENT NUMBER: 138:50651
TITLE: Identification and characterization of a second
novel human Erythrovirus variant, A6
AUTHOR(S): Nguyen, Quang Tri; Wong, Susan; Heegaard, Erik
D.; Brown, Kevin E.
CORPORATE SOURCE: Hematology Branch, National Heart, Lung, and
Blood Institute, Bethesda, MD, 20892, USA
SOURCE: Virology (2002), 301(2), 374-380
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Parvovirus B19 (B19), currently the only accepted member of the Erythrovirus genus, is the only parvovirus known to be pathogenic in humans. Recently a viral sequence, tentatively termed V9 which showed 11% variability from the published B19 sequences, was described from a patient with aplastic crisis. To search for addnl. parvovirus variants, we used the new NS1/7.5EC PCR assay whose primers were designed from a conserved region of the B19/V9 sequence and encompasses an MfeI restriction enzyme site that would allow differentiation between B19- and V9-like sequences. Screening of 225 serum and bone marrow samples and 62 plasma pools identified one new atypical parvovirus sequence, A6, from an anemic HIV-pos. patient. A6 exhibited 88% similarity to B19 and 92% to V9, compared to >98% correspondence between reported B19 isolates. Based on the genome similarity to B19, an RT-PCR for A6 capsid transcripts was

developed and used to test for A6 infectivity of UT7/Epo/S1 cells. Despite high viral titers, A6 viral transcripts were not detected. Thus, although the prevalence of B19 variants probably is low, the true clin. significance remains unknown. Current PCR analyses are unlikely to detect novel variants without the design of specific primers to the A6/V9/B19 common sequences.

IT 479479-66-8 479479-70-4

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; identification and characterization of second novel human Erythrovirus variant, A6)

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:674041 HCAPLUS

DOCUMENT NUMBER: 137:364072

TITLE: Genetic diversity within human erythroviruses: identification of three genotypes

AUTHOR(S): Servant, Annabelle; Laperche, Syria; Lallemand, Francis; Marinho, Valerie; De Saint Maur, Guillemette; Meritet, Jean Francois; Garbarg-Chenon, Antoine

CORPORATE SOURCE: Laboratoire de Virologie, Hopital Armand Trousseau (EA2391, UFR Saint-Antoine, Paris, 75571, Fr.

SOURCE: Journal of Virology (2002), 76(18), 9124-9134
CODEN: JOVIAM; ISSN: 0022-538X

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB B19 virus is a human virus belonging to the genus Erythrovirus. The genetic diversity among B19 virus isolates has been reported to be very low, with less than 2% nucleotide divergence in the whole genome sequence. We have previously reported the isolation of a human erythrovirus isolate, termed V9, whose sequence was markedly distinct (>11% nucleotide divergence) from that of B19 virus. To date, the V9 isolate remains the unique representative of a new variant in the genus Erythrovirus, and its taxonomic position is unclear. We report here the isolation of 11 V9-related viruses. A prospective study conducted in France between 1999 and 2001 indicates that V9-related viruses actually circulate at a significant frequency (11.4%) along with B19 viruses. Anal. of the nearly full-length genome sequence of one V9-related isolate (D91.1) indicates that the D91.1 sequence clusters together with but is notably distant from the V9 sequence (5.3% divergence) and is distantly related to B19 virus sequences (13.8 to 14.2% divergence). Addnl. phylogenetic anal. of partial sequences from the V9-related isolates combined with erythrovirus sequences available in GenBank indicates that the erythrovirus group is more diverse than thought previously and can be divided into three well-individualized genotypes, with B19 viruses corresponding to genotype 1 and V9-related viruses being distributed into genotypes 2 and 3.

IT 475116-54-2, Protein VP1 (B19 virus strain D91.1)

475116-56-4, Protein VP2 (B19 virus strain D91.1)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

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(amino acid sequence; genetic diversity among human
erythroviruses including 11 new isolates of V9-related
erythroviruses)

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 7 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:572038 HCAPLUS

DOCUMENT NUMBER: 137:104826

TITLE: Identification of essential genes in prokaryotes
and use of their antisense constructs in
antibiotic screening

INVENTOR(S): Roemer, Terry; Jiang, Bo; Boone, Charles;
Bussey, Howard; Ohlsen, Kari L.

PATENT ASSIGNEE(S): Elitra Pharmaceuticals, Inc., USA

SOURCE: PCT Int. Appl., 167 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002053728	A2	20020711	WO 2001-XA49486	20011226
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2000-259128P P 20001229

US 2001-792024 A 20010220

US 2001-314050P P 20010822

AB The present invention provides methods and compns. that enable the exptl. determination as to whether any gene in the genome of a diploid pathogenic organism is essential, and whether it is required for virulence or pathogenicity. The methods involve the construction of genetic mutants in which one allele of a specific gene is inactivated while the other allele of the gene is placed under conditional expression. The identification of essential genes and those genes critical to the development of virulent infections, provides a basis for the development of screens for new drugs against such pathogenic organisms. The present invention further provides *Candida albicans* genes that are demonstrated to be essential and are potential targets for drug screening. The nucleotide sequence of the target genes can be used for various drug discovery purposes, such as expression of the recombinant protein, hybridization assay and construction of nucleic acid arrays. The uses of proteins encoded by the essential genes, and genetically engineered cells comprising modified alleles of essential genes in various screening methods are also encompassed by the invention.

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The patent has clamid 7932 DNA and protein sequences, but the sequence information is not available upon the time of this publication.

IT 443165-89-7

RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses) (amino acid sequence; Identification of essential genes in prokaryotes and use of their antisense constructs in antibiotic screening)

L2 ANSWER 8 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:335528 HCAPLUS

DOCUMENT NUMBER: 133:1513

TITLE: Insertional mutagenesis of AAV2 capsid and the production of recombinant virus for gene therapy

INVENTOR(S): Rabinowitz, Joseph E.; Samulski, Richard Jude; Xiao, Weidong

PATENT ASSIGNEE(S): The University of North Carolina At Chapel Hill, USA

SOURCE: PCT Int. Appl., 153 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000028004	A1	20000518	WO 1999-US26505	19991110
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1135468	A1	20010926	EP 1999-962729	19991110
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
JP 2002538770	T2	20021119	JP 2000-581171	19991110
US 2003053990	A1	20030320	US 2002-205942	20020726
PRIORITY APPLN. INFO.:			US 1998-107840P	P 19981110
			US 1999-123651P	P 19990310
			US 1999-438268	A3 19991110
			WO 1999-US26505	W 19991110

AB The present invention provides genetically-engineered parvovirus capsids and viruses designed to introduce a heterologous gene into a target cell. The parvoviruses of the invention provide a repertoire of vectors with altered antigenic properties, packaging capabilities, and/or cellular tropisms as compared with current AAV vectors. The structural genes of adeno-associated virus serotype 2 (AAV2) have been altered by linker insertional mutagenesis (using RGD linker, bradykinin-linker, poly-lys linker, or poly-his linker) in order to define critical components of virion assembly and infectivity. Three classes of capsid mutants were identified by

assaying for capsid production, packaging, transduction, heparin agarose binding, and morphol. Class I mutants expressed structural proteins but are defective in virion assembly. Class II mutants generated intact virions that protected the viral genome from DNase, but failed to infect target cells, and the majority of these mutants bound the heparin affinity matrix. Finally, class III mutants assembled virions, encapsidated DNA, and infected target cells, and infectivity of these mutants ranged from 5 to 100% of that of the wild-type, demonstrating for the first time the ability to alter capsid proteins without interfering with infectivity. Chimeric AAV vector (AAV2/4 including VP3 loop swap hybrid viruses and B19/AAV2) and MSH-targeted AAV (by inserting MSH into AAV2 capsid protein loop 3) are generated and analyzed for their packaging capacities or target specificity. These recombinant AAV virions with altered capsid subunits are useful templates for cell-specific gene delivery in gene therapy or for vaccine development.

IT 270056-63-8

RL: PRP (Properties)

(unclaimed protein sequence; insertional Mutagenesis of AAV2 Capsid and the Production of Recombinant Virus for gene therapy)

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 9 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:243783 HCAPLUS

DOCUMENT NUMBER: 133:160443

TITLE: Integrity and full coding sequence of B19 virus DNA persisting in human synovial tissue

AUTHOR(S): Hokynar, Kati; Brunstein, John; Soderlund-Venermo, Maria; Kiviluoto, Olli; Partio, Esa K.; Konttinen, Yrjo; Hedman, Klaus
CORPORATE SOURCE: Department of Virology, Haartman Institute, University of Helsinki, Helsinki, FIN-00014, Finland

SOURCE: Journal of General Virology (2000), 81(4), 1017-1025

CODEN: JGVIAY; ISSN: 0022-1317

PUBLISHER: Society for General Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Primary infection by human parvovirus B19 is often accompanied by arthropathy of varying duration, of which the most severe cases can be indistinguishable from rheumatoid arthritis (RA). While this might seem to imply a role in RA pathogenesis, recent studies have verified long-term persistence of B19 DNA in synovial tissue not only in patients with rheumatoid or juvenile arthritis, but also in immunocompetent, non-arthritic individuals with a history of prior B19 infection. However, the latter data are based on PCR amplification of short segments of DNA, with little sequence information. We determined the nucleotide sequence and examined the integrity of the protein-coding regions of B19 genomes persisting in synovial tissue and compared the results with data from synovial tissues of recently infected patients. In synovium of both previously and recently infected subjects, the viral coding regions were found to be present in an apparently continuous, intact DNA mol. Comparison with sequences reported from blood or bone marrow showed that the synoviotropism or persistence of the B19 virus DNA

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was not due to exceptional mutations or particular genotype variants. The synovial retention of full-length viral genomes may represent a physiol. process functioning in long-term storage of foreign macromols. in this tissue.

IT 287950-53-2 287984-41-2 287984-42-3

287984-43-4

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; partial sequence of B19 virus capsid protein VP1 isolated from human synovial tissue)

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 10 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:375643 HCAPLUS

DOCUMENT NUMBER: 131:28643

TITLE: Erythrovirus V9 and methods for its detection

INVENTOR(S): Nguyen, Quang Tri; Garbarg-Chenon, Antoine; Auguste, Veronique

PATENT ASSIGNEE(S): Assistance Publique-Hopitaux de Paris, Fr.

SOURCE: PCT Int. Appl., 77 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: French

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9928439	A2	19990610	WO 1998-FR2615	19981203
WO 9928439	A3	19990722		
W:	AL, AU, BA, BB, BG, BR, CA, CN, CU, CZ, EE, GD, GE, HR, HU, ID, IL, IS, JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SD, SG, SI, SK, SL, TR, TT, UA, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
FR 2771751	A1	19990604	FR 1997-15197	19971203
FR 2771751	B1	20000526		
CA 2311297	AA	19990610	CA 1998-2311297	19981203
AU 9914403	A1	19990616	AU 1999-14403	19981203
AU 757453	B2	20030220		
EP 1037916	A2	20000927	EP 1998-958322	19981203
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI			
JP 2001525163	T2	20011211	JP 2000-523317	19981203
PRIORITY APPLN. INFO.:			FR 1997-15197 A	19971203
			WO 1998-FR2615 W	19981203

AB The invention concerns nucleic sequences derived from human erythrovirus V9, a genetic variant of the B19 strain, and proteins encoded by V9 as well as their applications as diagnostic reagents and as immunogenic agents.

IT 226937-08-2 226937-14-0

RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)

(amino acid sequence; erythrovirus V9 and methods for its

detection)

L2 ANSWER 11 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1996:679256 HCAPLUS

DOCUMENT NUMBER: 126:2046

TITLE: Genetic diversity of human parvovirus B19:
sequence analysis of the VP1/VP2 gene from
multiple isolatesAUTHOR(S): Erdman, Dean D.; Durigon, Edison L.; Wang,
Qi-Yun; Anderson, Larry J.CORPORATE SOURCE: Div. Viral Rickettsial Diseases, Natl. Cent.
Infectious Diseases, Atlanta, GA, 30333, USASOURCE: Journal of General Virology (1996), 77(11),
2767-2774

CODEN: JGVIAY; ISSN: 0022-1317

PUBLISHER: Society for General Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB To evaluate the genetic variability of human parvovirus B19, the complete coding region of the VP1/VP2 structural proteins of 29 B19 isolates obtained from 25 infected patients were sequenced and compared with each other and with two previously published B19 isolates. The VP1/VP2 gene was amplified by PCR using B19-specific oligonucleotide primers and the amplification products were sequenced directly. Overall, the average nucleotide and predicted amino acid identity among B19 isolates was high. Sequential virus isolates from the same cases and isolates obtained from two cases linked by transmission in the same household were essentially identical. Sequence variation was minimal among isolates obtained from a single community-wide B19 outbreak, ranging between 0 and 10 (0.4%) base substitutions, although there appeared to be more than one genetic lineage circulating in the outbreak. A comparison with 18 addnl. isolates from distinct epidemiol. settings found greater variability. These isolates differed from each other by between 11 (0.5%) and 112 (4.8%) base substitutions. B19 isolates from Xi'an, China, were significantly different from other isolates at both the nucleotide and amino acid levels, and were more closely related to a single isolate from Japan, obtained 10 yr earlier, than to isolates from other countries. Isolates examined in this study included distinct genotypes from patients with similar clin. presentations and similar genotypes from patients with diverse clin. presentations. These data suggest that geog. defined genetic lineages of B19 may exist and that no particular B19 genotype was associated with a particular clin. outcome.

IT 181380-31-4 183389-77-7, Protein VP1 (B19 virus strain USA2) 183389-78-8, Protein VP1 (B19 virus strain USA4) 183389-79-9, Protein VP1 (B19 virus strain USA5)

183389-80-2, Protein VP1 (B19 virus strain UK1)

183389-81-3, Protein VP1 (B19 virus strain BRZ1)

183389-82-4, Protein VP1 (B19 virus strain VEN1)

183389-83-5, Protein VP1 (B19 virus strain KOR1)

183389-84-6, Protein VP1 (B19 virus strain KOR2)

183389-85-7, Protein VP1 (B19 virus strain JAP1)

183389-86-8, Protein VP1 (B19 virus strain CHI1)

183389-87-9, Protein VP1 (B19 virus strain CHI2)

183511-25-3, Protein VP1 (B19 virus strain USA3)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

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(genetic diversity of human parvovirus B19 VP1/VP2 gene from multiple isolates)

L2 ANSWER 12 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1996:538591 HCAPLUS

DOCUMENT NUMBER: 125:213792

TITLE: Sequence analysis of a parvovirus B19 isolate and baculovirus expression of the non-structural protein

AUTHOR(S): Hicks, K. E.; Cubel, R. C. N.; Cohen, B. J.; Clewley, J. P.

CORPORATE SOURCE: Virus Reference Division, Central Public Health Laboratory, London, UK

SOURCE: Archives of Virology (1996), 141(7), 1319-1327
CODEN: ARVIDF; ISSN: 0304-8608

PUBLISHER: Springer

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Serol. for parvovirus B19 has been hampered by limited availability of antigen which has often had to be isolated from viremic blood donations. We have determined the sequence of the genome of one such isolate (Stu). It is 99% similar to the sequences of two other isolates (Wi and Au) except at the far 5'-end, where it is more similar to the terminus of another isolate (Ala/Alb). Recombinant nonstructural protein, NS, was constructed. Antibodies to NS, as well as to the capsid proteins, VP1/2, were detected in patients with B19 infection.

IT 181380-31-4

RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses) (amino acid sequence; of parvovirus B19 isolate and baculovirus expression of the non-structural protein)

L2 ANSWER 13 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1995:781962 HCAPLUS

DOCUMENT NUMBER: 123:190542

TITLE: Human parvovirus antigen proteins VP-1 and VP-2 and NS and cloning and expression of their genes
INVENTOR(S): Yamazaki, Osamichi; Matsunaga, Yasuko; Takeda, Naokazu; Matsura, Zenji; Ogawa, Hiroyuki; Shimizu, Hideharu; Kamata, Kunio; Kurosawa, Daisuke

PATENT ASSIGNEE(S): Denki Kagaku Kogyo Kk, Japan; Denka Seiken Kk

SOURCE: Jpn. Kokai Tokkyo Koho, 38 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 07147986	A2	19950613	JP 1992-281017	19920924
PRIORITY APPLN. INFO.:			JP 1992-281017	19920924

AB A DNA encoding the human parvovirus antigen proteins VP-1 and VP-2 and NS (nonstructural) was cloned and sequenced. These 3 proteins contained 781, 554, and 671 amino acids, resp. These encoded proteins were used in immuno-detection of anti-human parvovirus

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antibodies and for detection of human parvovirus. Based on this cloned DNA, DNA primers were devised and the polymerase chain reaction was used for the detection of human parvovirus.

IT 167614-99-5 167615-00-1

RL: PRP (Properties)

(amino acid sequence; human parvovirus antigen proteins VP-1 and VP-2 and NS and cloning and expression of their genes)

L2 ANSWER 14 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1992:19653 HCAPLUS

DOCUMENT NUMBER: 116:19653

TITLE: Immunogenic peptides of parvovirus B19

INVENTOR(S): Soutschek, Erwin; Motz, Manfred

PATENT ASSIGNEE(S): Mikrogen Molekularbiologische
Entwicklungs-G.m.b.H., Germany

SOURCE: Ger. Offen., 21 pp.

CODEN: GWXXBX

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 4003826	A1	19910814	DE 1990-4003826	19900208
DE 4003826	C2	19951123		
CA 2075366	AA	19910809	CA 1991-23075366	19910208
WO 9112269	A1	19910822	WO 1991-DE106	19910208
W: AU, CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
AU 9172115	A1	19910903	AU 1991-72115	19910208
AU 650864	B2	19940707		
EP 514413	A1	19921125	EP 1991-903270	19910208
EP 514413	B1	19940504		
R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE				
JP 05504143	T2	19930701	JP 1991-503659	19910208
JP 3061196	B2	20000710		
AT 105303	E	19940515	AT 1991-903270	19910208
ES 2052370	T3	19940701	ES 1991-903270	19910208
CA 2075366	C	20030218	CA 1991-2075366	19910208
US 6274307	B1	20010814	US 1997-856841	19970515
JP 2000184889	A2	20000704	JP 2000-17931	20000124
JP 3130024	B2	20010131		

PRIORITY APPLN. INFO.:

DE 1990-4003826	A	19900208
WO 1991-EP106	W	19910121
EP 1991-903270	A	19910208
JP 1991-503659	A3	19910208
WO 1991-DE106	A	19910208
US 1992-917096	B2	19920804
US 1994-214658	B1	19940316

AB The title peptides, preferably containing 8-50 amino acids, contain at least part of the amino acid sequence of the UP1 or UP2 capsid protein of parvovirus B19. They are used for detection of antibodies to B19 and for vaccines. Mol. cloning of VP1 and VP2, and isolation of various fragments, is presented. Amino acid sequences of the fragments are given. Synthetic peptides are also described.

IT 138158-34-6

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RL: PROC (Process)

(amino acid sequence and mol. cloning of, for diagnosis and vaccines)

IT 138158-32-4

RL: BIOL (Biological study)

(amino acid sequence and mol. cloning of, of parvovirus B19, diagnosis and vaccines in relation to)

L2 ANSWER 15 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1986:455398 HCAPLUS

DOCUMENT NUMBER: 105:55398

TITLE: Nucleotide sequence and genome organization of human parvovirus B19 isolated from the serum of a child during aplastic crisis

AUTHOR(S): Shade, Rosemary O.; Blundell, Matthew C.; Cotmore, Susan F.; Tattersall, Peter; Astell, Caroline R.

CORPORATE SOURCE: Fac. Med., Univ. British Columbia, Vancouver, BC, V6T 1W5, Can.

SOURCE: Journal of Virology (1986), 58(3), 921-36

CODEN: JOVIAM; ISSN: 0022-538X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The nucleotide sequence of an almost-full-length clone of human parvovirus B19 was determined. Whereas the extreme left and right ends of this genomic clone are incomplete, the sequence clearly indicates that the 2 ends of viral DNA are related by inverted terminal repeats similar to those of the Dependovirus genes. The coding regions are complete in the cloned DNA, and the 2 large open reading frames which span almost the entire genome are restricted to 1 strand, as has been found for all other parvoviruses characterized to date. From the DNA sequence it is concluded that the organization of the B19 transcription units is similar, although not identical, to those of other parvoviruses. In particular, the B19 genome may utilize a 4th promoter to transcribe mRNA encoding the major structural polypeptide, VP2. Anal. of the putative polypeptides confirms that B19 is only distantly related to the other parvoviruses but reveals that there is a small region in the gene probably encoding the major nonstructural protein of B19 that is closely conserved between all of the parvovirus genomes for which sequence information is currently available.

IT 103351-69-5

RL: PRP (Properties)

(amino acid sequence of)

E1 THROUGH E46 ASSIGNED

FILE 'REGISTRY' ENTERED AT 14:13:00 ON 20 JAN 2004

L3 46 SEA FILE=REGISTRY ABB=ON PLU=ON (181380-31-4/BI OR 103351-69-5/BI OR 138158-32-4/BI OR 138158-34-6/BI OR 167614-99-5/BI OR 167615-00-1/BI OR 183389-77-7/BI OR 183389-78-8/BI OR 183389-79-9/BI OR 183389-80-2/BI OR 183389-81-3/BI OR 183389-82-4/BI OR 183389-83-5/BI OR 183389-84-6/BI OR 183389-85-7/BI OR 183389-86-8/BI OR 183389-87-9/BI OR 183511-25-3/BI OR 226937-08-2/BI OR 226937-14-0/BI OR 270056-63-8/BI OR 287950-53-2/BI OR 287984-41-2/BI OR 287984-42-3/BI OR 287984-43-4/BI OR 443165-89-7/BI OR 475116-54-2/BI OR 475116-56-4/BI OR

Searcher : Shears 571-272-2528

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479479-66-8/BI OR 479479-70-4/BI OR 482672-19-5/BI OR
482672-21-9/BI OR 482672-25-3/BI OR 482672-27-5/BI OR
488188-04-1/BI OR 488188-05-2/BI OR 488188-07-4/BI OR
488188-08-5/BI OR 488728-12-7/BI OR 488728-13-8/BI OR
488728-14-9/BI OR 488728-15-0/BI OR 488728-16-1/BI OR
488728-17-2/BI OR 488728-60-5/BI OR 604833-49-0/BI)

L4 46 L1 AND L3

L4 ANSWER 1 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 604833-49-0 REGISTRY
CN Protein (Candida albicans gene CaYPL204W) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2434: PN: US20030180953 SEQID: 7570 claimed protein
CI MAN
SQL 433

SEQ 1 MDLRVGKKYR IGRKIGSGSF GDIYLG TNII SGEEVAIKLE NTKAKHPQLE
51 YEAKVYKALS GGVGIPFVRW YGTECDYNAM VIDLLGPSLE DLFNYCNRK F
101 TYKTVLLAD QLICRIEYIH ARCFIHRDIK PDNFLMGIGR RGSQVNVIDF
151 GLAKKYRDPR THLHIPYREN KNLTGTARYA SVNTHLGIEQ SRRDDLES LG
201 YVLIYFCRGS LPWQGLKAAT KRQKYDRIME KKM TTPNNIL CKGLPSEFLE
251 YMNYVKTLRF DDKPDYPYLR KLF RD LFKKE NYRYDYVFDW TLYKFQQEKQ
301 RAQQGKVADG DNQDQQQQQN NQNQTQTQNO QGQITAPQPP VPVSQQQQQQ
351 QQIPQHIPTP QQISQQQQQQ QQQQQQLPPQ QQKTSVTPQL QQYTDQRLQN
=====

401 QRAVYQSNQN YSGTKSAQPQ AQQPPQGNP AWL
HITS AT: 391-396

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:272071

L4 ANSWER 2 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488728-60-5 REGISTRY
CN L-Methionine, L-threonyl-L-tyrosyl-L-phenylalanyl-L-prolyl-L-
asparaginyl-L-lysylglycyl-L-threonyl-L-glutaminy l-L-glutaminy l-L-
tyrosyl-L-threonyl-L- α -aspartyl-L-glutaminy l-L-isoleucyl-L-
 α -glutamyl-L-arginyl-L-prolyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 48: PN: US20030017596 SEQID: 48 claimed sequence
SQL 20

SEQ 1 TYFPNKG TQQ YTDQIERPLM
=====

HITS AT: 5-14

REFERENCE 1: 138:103553

L4 ANSWER 3 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488728-17-2 REGISTRY
CN L-Glutamine, L-glutaminy l-L-glutaminy l-L-tyrosyl-L-threonyl-L-
 α -aspartyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: US20030017596 SEQID: 7 claimed sequence
SQL 6

SEQ 1 QQYTDQ

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=====

HITS AT: 1-6

REFERENCE 1: 138:103553

L4 ANSWER 4 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488728-16-1 REGISTRY
CN L-Threonine, L-asparaginyl-L-lysylglycyl-L-threonyl-L-glutaminyl-L-glutaminyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 6: PN: US20030017596 SEQID: 6 claimed sequence
SQL 8

SEQ 1 NKGTQQYT
=====

HITS AT: 1-8

REFERENCE 1: 138:103553

L4 ANSWER 5 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488728-15-0 REGISTRY
CN L-Glutamine, L-asparaginyl-L-lysylglycyl-L-threonyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-threonyl-L- α -aspartyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 5: PN: US20030017596 SEQID: 5 claimed sequence
SQL 10

SEQ 1 NKGTQQYTDQ
=====

HITS AT: 1-10

REFERENCE 1: 138:103553

L4 ANSWER 6 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488728-14-9 REGISTRY
CN L-Glutamic acid, L-asparaginyl-L-lysylglycyl-L-threonyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-isoleucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: US20030017596 SEQID: 4 unclaimed sequence
SQL 12

SEQ 1 NKGTQQYTDQ IE
=====

HITS AT: 1-10

REFERENCE 1: 138:103553

L4 ANSWER 7 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488728-13-8 REGISTRY
CN L-Glutamic acid, L-threonyl-L-tyrosyl-L-phenylalanyl-L-prolyl-L-asparaginyl-L-lysylglycyl-L-threonyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-isoleucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3: PN: US20030017596 SEQID: 3 unclaimed sequence
SQL 16

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SEQ 1 TYFPNKGTTQ YTDQIE

=====

HITS AT: 5-14

REFERENCE 1: 138:103553

L4 ANSWER 8 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN

RN 488728-12-7 REGISTRY

CN L-Glutamic acid, glycyl-L-leucyl-L-asparaginyl-L-methionyl-L-histidyl-L-threonyl-L-tyrosyl-L-phenylalanyl-L-prolyl-L-asparaginyl-L-lysylglycyl-L-threonyl-L-glutaminyl-L-glutaminyl-L-tyrosyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-isoleucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2: PN: US20030017596 SEQID: 2 unclaimed sequence

SQL 21

SEQ 1 GLNMHTYFPN KGTTQYTDQI E

= =====

HITS AT: 10-19

REFERENCE 1: 138:103553

L4 ANSWER 9 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN

RN 488188-08-5 REGISTRY

CN Protein VP2 (B19 virus strain HaAM gene VP2 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAK95575

CN GenBank AAK95575 (Translated from: GenBank AY044268)

CI MAN

SQL 546

SEQ 1 MTSVNSAEAS TGAGGGGSGNP VKSMWSEGAT FTANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQH LIEN YGSIAPDALT VTISEIAVKD VTDKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGQQQDTL APELPIWVYF PPQYAYLTVG DVNTQGIGSD
201 SKKLASEESA FYVLEHSSFE LLGTGGSATM SYKFPPVPPE NLEGCSQHFY
251 EMYNPLYGSR LGVPDTLGGD PKFRSLTHED HAIQPQNFMP GPLVNSVSTK
301 EGDSSNTGAG KALTGLSTGT SQSTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQGLNIH TYFPNKGTTQ

=====

401 YTDQIERPLM VGSVWNRRL HYESQLWSKI PNLNDSFKTH FAALGGWGLH

=====

451 QPPPQIFLKI LPQSGPIGGI KSMGITTIVQ YAVGIMTVTI TFKLGPRKAT

501 GRWNPQPGVY PPHAAGHLPY VLYDPTATDA KQHHRHGYEK PEELWT

HITS AT: 395-404

REFERENCE 1: 138:164464

L4 ANSWER 10 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN

RN 488188-07-4 REGISTRY

CN Protein VP1 (B19 virus strain HaAM gene VP1 N-terminal fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAK95574

CN GenBank AAK95574 (Translated from: GenBank AY044268)

Searcher : Shears 571-272-2528

09/991433

CI MAN
SQL 773

SEQ 1 MSKESGKWWE SDDKFAKDVY KQFVEFYKKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKSNL KDSPDLYSHH FQSHGQLSDH PHALSPSSSH
101 TEPRGENAVL SSDDLHKPGQ VSIQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQI AKLGINPYTH WTVADEELLK NIKNETGFQA QAVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVTI KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFELLG
451 TGGSATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPGL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQS
551 TRISLRPGPV SQPYHHWDTI KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNIHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL NDSFKTHFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTITFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWT

HITS AT: 622-631

REFERENCE 1: 138:164464

L4 ANSWER 11 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488188-05-2 REGISTRY
CN Protein VP2 (B19 virus strain LaLi gene VP2 N-terminal fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAK95572
CN GenBank AAK95572 (Translated from: GenBank AY044266)
CI MAN
SQL 546

SEQ 1 MTSVNSAEAS TGAGGGGSGNP VKSMWSEGAT FTANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQHLENI YGSIAPDALI VTISEIAVKD VTDKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGQGQDTL APELPIWVYF PPQYAYLTVG DVNTQGISGD
201 SKKLASEESA FYVLEHSSFE LLGTGGSATM SYKFPPVPPE NLEGCSQHFY
251 EMYNPLYGSR LGVPDTLGGD PKFRSLTHED HAIQPQNFMP GPLVNSVSTK
301 EGDTSNTGAG KALTGLSTGT SQSTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQGLNIH TYFPNKGTTQ
===== =
401 YTDQIERPLM VGSVWNRRAL HYESQLWSKI PNLDDSFKTQ FAALGGWGLH
=====
451 QPPPQIFLKI LPQSGPIGGI KSMGITTIVQ YAVGIMVTM TFKLGPRKAT
501 GRWNPQPGVY PPHAAGHLPY VLYDPTATDA KQHHRHGYEK PEELWT

HITS AT: 395-404

REFERENCE 1: 138:164464

L4 ANSWER 12 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 488188-04-1 REGISTRY
CN Protein VP1 (B19 virus strain LaLi gene VP1 N-terminal fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAK95571
CN GenBank AAK95571 (Translated from: GenBank AY044266)

09/991433

CI MAN
SQL 773

SEQ 1 MSKESGKWE SDDKFAKDVY KQFVEFYKKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKSNL KDSPDLYSHH FQSHGQLSDH PHALSPSSSH
101 TEPRGENAVL SSDDLHKPGQ VSIQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QAVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSPVKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFELLG
451 TGGSATMSYK FPPVPPENLE GCSQHFIYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD TSNTGAGKAL TGLSTGTSQS
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNIHTYF PNKGTQOYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWT

HITS AT: 622-631

REFERENCE 1: 138:164464

L4 ANSWER 13 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 482672-27-5 REGISTRY
CN Protein VP2 (B19 virus clone 2-B6) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 35: PN: WO03002753 SEQID: 35 claimed protein
CI MAN
SQL 554

SEQ 1 MTSVNSAEAS TGAGGGGSGNP VKSMWSEGAT FSANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQHLENI YGSIAPDALT VTISEIAVKD VTNKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGQGQDTL APELPIWVYF PPQYAYLTVG DVNTQGISGD
201 SKKLASEESA FYVLEHSSFQ LLGTGGTATM SYKFPPVPPE NLEGCSQHFY
251 EMYNPLYGSR LGVPDTLGGD PKFRSLTHED HAIQPQNFMPL GPLVNSVSTK
301 EGDSSSTGAG KALTGLSTGT SQNTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQGLNMH TYFPNKGTOQ
===== =
401 YTDQIERPLM VGSVWNRRAL HYESQLWSKI PNLDDSFKTQ FAALGGWGLH
=====
451 QPPPQIFLKI LPQSGPIGGI KSMGITTIVQ YAVGIMVTM TFKLGPRKAT
501 GRWNPQPGVY PPHAAGHLPY VLYDPTATDA QHHRHGYEK PEELWTAKSR
551 VHPL

HITS AT: 395-404

REFERENCE 1: 138:84433

L4 ANSWER 14 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 482672-25-3 REGISTRY
CN Protein VP1 (B19 virus clone 2-B6) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 33: PN: WO03002753 SEQID: 33 claimed protein
CI MAN
SQL 781

09/991433

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGEDAVL SSDDLHKPGQ VSVQLPGTNY VGPGLNELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPMSMTS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFESPLE FQHLIENYGS IAPDALTVTI
351 SEIAVKDVTN KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD SSSTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHOPP PQIFLKILPQ SGPIGGIKSM
701 GITTLLVQYAV GIMTVMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
HITS AT: 622-631

REFERENCE 1: 138:84433

L4 ANSWER 15 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 482672-21-9 REGISTRY
CN Protein VP2 (B19 virus clone 2-B1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 29: PN: WO03002753 SEQID: 29 claimed protein
CI MAN
SQL 554

SEQ 1 MTSVNSAEAS TGAGGGGSGNP VKSMWSEGAT FSANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQHLIEN YGSIAPDALT VTISEIAVKD VTDKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGQGQDTL APELPIWVYF PPQYAYLTVG DVNTQGISGD
201 SKKLASEESA FYVLEHSSFQ LLGTGGTATM SYKFPVPPE NLEGCSQHFY
251 EMYNPLYGSR LGVPDTLGGD PKFRSLTHED HAIQPQNEMP GPLVNSVSTK
301 EGDSSSTGAG KALTGLSTGT SQNTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQGLNMH TYFPNKGTTQ
===== =
401 YTDQIERPLM VGSVWNRRAL HYESQLWSKI PNLDDSKTQ FAALGGWGLH
=====
451 QPPPQIFLKI LPQSGPIGGI KSMGITTLLVQ YAVGIMTVTM TFKLGPRKAT
501 GRWNPQPGVY PPHAAGHPY VLYDPTATDA KQHHRHGYEK PEELWTAKSR
551 VHPL
HITS AT: 395-404

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:84433

L4 ANSWER 16 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 482672-19-5 REGISTRY
CN Protein VP1 (B19 virus clone 2-B1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 27: PN: WO03002753 SEQID: 27 claimed protein
CI MAN
SQL 781

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD

09/991433

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51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSH
101 AEPRGEDAVL SSDDLHKPGQ VSVQLPGTNY VPGNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQHLENIYGS IAPDALVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD SSSTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
=====
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTIVQYAV GIMTVMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
```

HITS AT: 622-631

REFERENCE 1: 138:84433

L4 ANSWER 17 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 479479-70-4 REGISTRY
CN Protein (Erythrovirus A6 clone c8 7.5-kilodalton) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAL55422
CN GenBank AAL55422 (Translated from: GenBank AY064476)
CI MAN
SQL 781

```
SEQ 1 MSKKSDKWWE SDDKFAKDVY KQFVEFYEKV TETDLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLFDH PHALSPSSSH
101 TEPRGEDAVL SSDDLHKPGR VSIQLPGTNY IGPNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QAVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQHLENIYGS IAPDALVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFELLG
451 TGGSATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD TSNTGAGKAL TGLSTGTSQS
551 TRISLRPGPV SQPYHYWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNIHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
=====
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTIVQYAV GIMTVMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDANQH HKHGYEKPEE LWTAKSRVHP L
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HITS AT: 622-631

REFERENCE 1: 138:50651

L4 ANSWER 18 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 479479-66-8 REGISTRY
CN Protein (Erythrovirus A6 clone c2 7.5-kilodalton) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAL55418
CN GenBank AAL55418 (Translated from: GenBank AY064475)

09/991433

CI MAN
SQL 781

SEQ 1 MSKKSDKWWE SDDKFAKDVY KQFVEFYEKV TETDLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKSNL KOTPDLYSHH FQSHGQLFDH PHALSPSSSH
101 TEPRGEDAVL SSDDLHKPGQ VSIQLPGTNY IGPGLNELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QAVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSPNVKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYEPHR YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLLIENYGS IAPDALVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTAGDVN TQGISGDSKK LASEESAFYV LEHSSFELLG
451 TGGSATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDLGGDPKF
501 RSLTHEDHAI QPQNFMGPGL VNSVSTKEGD TSNTGAGKAL TGLSTGTSQS
551 TRISLRPGPV SQPYHHWTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNIHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 138:50651

L4 ANSWER 19 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 475116-56-4 REGISTRY
CN Protein VP2 (B19 virus strain D91.1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAL91014
CN GenBank AAL91014 (Translated from: GenBank AY083234)
CI MAN
SQL 554

SEQ 1 MTSVNSAEAS TGAGGGGSGNP TKSMWSEGAT FTANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQHLLIEN YGSIAPDALT VTISEIAVKD VTDKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGGQDQTL APELPIWVYF PPQYAYLTVG EVNTQGVSGD
201 SKKLASEESA FYVLEHSSFQ LLGTGGSATM SYKFPVAVPE NLEGCSQHFY
251 EMINPLYGSR LGVPDTLGGD PKFRSLTHED HAIQPQNFM GPPLNSVSTK
301 EGDTSNTGAG KALTGLSTGT SQSTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQGLNMH TYFPNKGTQQ
===== =
401 YTDQIERPLM VGSVWNRRAL HYESQLWSKI PNLDDSKFTQ FAALGGWGLH
=====
451 QPPPQIFLKI LPQSGPIGGI KSMGITTIVQ YAVGIMTVM TFKLGPRKAT
501 GRWNPQPGVY PPHAAGHLPY VLYDPTATDA KQHRRHGYEK PEELWTAKSR
551 VHPL

HITS AT: 395-404

REFERENCE 1: 137:364072

L4 ANSWER 20 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 475116-54-2 REGISTRY
CN Protein VP1 (B19 virus strain D91.1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAL91013
CN GenBank AAL91013 (Translated from: GenBank AY083234)
CI MAN

09/991433

SQL 781

SEQ 1 MSKTTDRWWE SNTDFAQDVY KQFVQFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKSNL KNSPDLYSHH FQSHGQLSDH PHALSSSNSS
101 TEPRGENAVL SNEDLHKPGQ VSMQLPGTNY VGPGNELQAG PPQNAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QAVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPTKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLLIENYGS IAPDALTVTI
351 SEIAVKDVTG KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGEVN TQGVSGDSKK LASEESAFYV LEHSSFQLLG
451 TGGSATMSYK FPAVPPENLE GCSQHFYEMY NPLYGSRLGV PDLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL INSVSTKEGD TSNTGAGKAL TGLSTGTSQS
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTIVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 137:364072

L4 ANSWER 21 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 443165-89-7 REGISTRY
CN Protein (Candida albicans clone Sa386383_7570 gene fragment) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 570: PN: WO02053728 SEQID: 7570 claimed protein

CI MAN

SQL 433

SEQ 1 MDLRVGGKYR IGRKIGSGSF GDIYLGNTII SGEEVAIKLE NTKAKHPQLE
51 YEAKVYKALS GGVGIPFVRW YGTECDYNAM VIDLLGPSLE DLFNYCNRKF
101 TYKTVLLAD QLICRIEYIH ARCFIHRDIK PDNFLMGIGR RGSQVNVIFD
151 GLAKKYRDPR THLHIPYREN KNLTGTARYA SVNTHLGIEQ SRRDDLES LG
201 YVLIYFCRGS LPWQGLKAAT KRQKYDRIME KMTTPNNIL CKGLPSEFLE
251 YMNYVKTLRF DDKPDYPYLR KLFRDLFKKE NYRYDYVFDW TLYKFQQEKQ
301 RAQQGKVADG DNQDQQQQQN NQNQTQTQNO QGQITAPQPP VPVSQQQQQQ
351 QQIPQHIPTP QQISQQQQQQ QQQQQQLPPQ QQKTSVTPQL QQYTDQRLQN
=====
401 QRAVYQSNQN YSGTKSAQPQ AQQPPQGNP AWL

HITS AT: 391-396

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 137:104826

L4 ANSWER 22 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 287984-43-4 REGISTRY
CN Protein VP1 (B19 virus strain Kati3 N-terminal fragment) (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN GenBank AAD45915

CN GenBank AAD45915 (Translated from: GenBank AF161225)

CI MAN

SQL 765

09/991433

SEQ 1 MSKKSGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL ENSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSDDLHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPMSMTS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT D KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFXXXX XXXXXSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTLLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGY

HITS AT: 622-631

REFERENCE 1: 133:160443

L4 ANSWER 23 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 287984-42-3 REGISTRY
CN Protein VP1 (B19 virus strain Kati2 N-terminal fragment) (9CI) (CA
INDEX NAME)
OTHER NAMES:
CN GenBank AAD45912
CN GenBank AAD45912 (Translated from: GenBank AF161224)
CI MAN
SQL 760

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSDDLHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPMSMTS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT D KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFIYEMX XXXXXXXXLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLNQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTLLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH

HITS AT: 622-631

REFERENCE 1: 133:160443

L4 ANSWER 24 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 287984-41-2 REGISTRY
CN Protein VP1 (B19 virus strain Katil N-terminal fragment) (9CI) (CA
INDEX NAME)
OTHER NAMES:
CN GenBank AAD45910

09/991433

CN GenBank AAD45910 (Translated from: GenBank AF161223)
CI MAN
SQL 761

SEQ 1 MSKKSGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGEDAVL SSIDLHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALKLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT D KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYXXX XXXXXXRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH H

HITS AT: 622-631

REFERENCE 1: 133:160443

L4 ANSWER 25 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 287950-53-2 REGISTRY
CN Protein VP1 (B19 virus strain Kati4 N-terminal fragment) (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN GenBank AAD45917
CN GenBank AAD45917 (Translated from: GenBank AF161226)
CI MAN
SQL 769

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGEDAVL SSIDLHKPGQ VSVQLPGTAY VGPGNELQAG PPQSAIDSAA
151 RIHDFRYSLL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT D KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPE

HITS AT: 622-631

REFERENCE 1: 133:160443

L4 ANSWER 26 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 270056-63-8 REGISTRY

09/991433

CN 3: PN: WO0028004 APP: 4 unclaimed protein (9CI) (CA INDEX NAME)
CI MAN
SQL 756

SEQ 1 MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY
51 KYLGPFNGLD KGEPVNEADA AALEHDKAYD RQLDSGDNPY LKYNHADA EF
101 QERLKEDTSF GGNLGRAVFQ AKKRVLEPLG LVEEPVK TAP GK KRPVEHSP
151 VEPDSSSGTG KAGQQPARKR LNFGQTGDAD SVPDPQPLGQ PPAAPSG LGT
201 NTMTSVNSAE ASTGAGGGGS NSVKSMWSEG ATFSANSVTC TFSRQFLIPY
251 DPEHHYKVFS PAASSCHNAS GKEAKVCTIS PIMGYSTPWR YLDFNALNLF
301 FSPLEFQHLI ENYGSIAPDA LTVTISEIAV KDVTDKTGGG VQVTDSTTGR
351 LCMLVDHEYK YPYVLGQGQD TLAPELPIWV YFPPQYAYLT VGDVNTQGIS
401 GDSKKLASEE SAFYVLEHSS FQLLGTGCTA TMSYKFPPVP PENLEGCSQH
451 FYEMYNPLYG SRLGVPDTLG GDPKFRSLTH EDHAIQPQNF MPGPLVNSVS
501 TKEGDSSNTG AGKALTGLST GTSQNTRISL RGPVSPQPYH HWDTDKYVTG
551 INAISHGQTT YGNAEDKEYQ QGVGRFPNEK EQLKQLQLN MHTYFPNKGT
=====
601 QQYTDQIERP LMVGSVWNRR ALHYESQLWS KIPNLDDSEK TQFAALGGWG
=====
651 LHQPPPQIFL KILPQSGPIG GIKSMGITT L VQYAVGIMTV TMTFKLGPRK
701 ATGRWNPPQG VYPPHAAGHL PYVLYDPTAT DAKQHHRHGY EKPEELWTAK
751 SRVHPL

HITS AT: 597-606

REFERENCE 1: 133:1513

L4 ANSWER 27 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 226937-14-0 REGISTRY
CN Protein VP2 (erythrovirus strain V9 clone PCD.V9.C22) (9CI) (CA
INDEX NAME)
CI MAN
SQL 554

SEQ 1 MTSVNSAEAS TGAGGGG SNP TKSMWSEGAT FTANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQHLIEN YGSIAPDAL TISEIAVKD VTDKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGQGQDTL APELPIWVYF PPQYAYLTVG EVNTQGISGD
201 SKKLASEESA FYVLEHSSFE LLGTGGSATM SYKFPAVPPE NLEGCSQH FY
251 EMYNPLYGSR LGVPDTLG D PKFRSLTHED HAIQPQNFMP GPLINSVSTK
301 EGDNSNTGAG KALTGLSTGT SQNTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQLGLNMH TYFPNKGTQQ
=====
401 YTDQIERPLM VGSVWNRRAL HYESQLWSKI PNLDDSEK TQ FAALGGWGLH
=====
451 QPPPQIFLKI LPQSGPIGGI KSMGITT L VQ YAVGIMTV TMTFKLGPRKAT
501 GRWNPPQPGVY PPHAAGHLPY VLYDPTATDA KQHHRHGYEK PEELWTAKSR
551 VHPL

HITS AT: 395-404

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 131:28643

L4 ANSWER 28 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 226937-08-2 REGISTRY
CN Protein VP1 (erythrovirus strain V9 clone PCD.V9.C22) (9CI) (CA
INDEX NAME)
CI MAN

09/991433

SQL 781

```
SEQ      1 MSKTTNKWWE SSDKFAQDVY KQFVQFYEKA TGTDLLELIQI LKDHYNISLD
      51 NPLENPSSLF DLVARIKSNL KNSPDLYSHH FQSHGQLSDH PHALSSSNSS
     101 AEPRGENAVL SSEDHLKPGQ VSIQLPGTNY VGPGNELQAG PPQNAVDSAA
     151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QAVKDYFTLK
     201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPTKS
     251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
     301 VCTISPIMGY STPWRYLDFN ALNLFFSPLF FQHLENIYGS IAPDALTVTI
     351 SEIAVKDVTD KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
     401 LPIWVYFPPQ YAYLTVGEVN TQGISGDSKK LASEESAFYV LEHSSFELLG
     451 TGGSATMSYK FPAVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
     501 RSLTHEDHAI QPQNFMGPGL INSVSTKEGD NSNTGAGKAL TGLSTGTSQN
     551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
     601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
          =====
     651 SQLWSKIPNL DDSFKTQFAA LGGWGLHOPP PQIFLKILPQ SGPIGGIKSM
     701 GITTIVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
     751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
```

HITS AT: 622-631

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 131:28643

L4 ANSWER 29 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183511-25-3 REGISTRY
CN Protein VP1 (B19 virus strain USA3) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47797
CN GenBank AAB47797 (Translated from: GenBank U38515)
CN Protein VP1/VP2 (human parvovirus B19 strain USA3)
CI MAN
SQL 781

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SEQ      1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
      51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSH
     101 AEPRGENAVL SSEDHLKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
     151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
     201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
     251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
     301 VCTISPIMGY STPWRYLDFN ALNLFFSPLF FQHLENIYGS IAPDALTVTI
     351 SEIAVKDVTD KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
     401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
     451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
     501 RSLTHEDHAI QPQNFMGPGL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
     551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
     601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
          =====
     651 SQLWSKIPNL DDSFKTQFAA LGGWGLHOPP PQIFLKILPQ SGPIGGIKSM
     701 GITTIVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
     751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
```

HITS AT: 622-631

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 126:2046

09/991433

L4 ANSWER 30 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-87-9 REGISTRY
CN Protein VP1 (B19 virus strain CHI2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47789
CN GenBank AAB47789 (Translated from: GenBank U38507)
CN Protein VP1/VP2 (human parvovirus B19 strain CHI2)
CI MAN
SQL 781

SEQ 1 MSKESGKWE SDDKFAKAVY QQFVEFYEKL TGTDLLELIQI LKDHYNISLD
51 HPLENPSSLF DLVARIKHNH KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGEDAVL SSED LHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQ LAKGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSADASTGA GGGGSNPVKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFPSPLE FQHLIENYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP E
401 LPIWVYFPPQ YAYLTVGDVN TQGIGDSKK LASEESAFYV LEHSSFQLLG
451 TGGASMSYK FPAVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAV QPQNFMPGPL VNSVSTKEGD NSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHEPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 31 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-86-8 REGISTRY
CN Protein VP1 (B19 virus strain CHI1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47788
CN GenBank AAB47788 (Translated from: GenBank U38506)
CN Protein VP1/VP2 (human parvovirus B19 strain CHI1)
CI MAN
SQL 781

SEQ 1 MSKESGKWE SDDKFAKAVY QQFVEFYEKL TGTDLLELIQI LKDHYNISLD
51 HPLENPSSLF DLVARIKHNH KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGEDAVL SSED LHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQ LAKGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSADASTGA GGGGSNPVKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFPSPLE FQHLIENYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP E
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTASMSYK FPAVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNIHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

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HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 32 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-85-7 REGISTRY
CN Protein VP1 (B19 virus strain JAP1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47791
CN GenBank AAB47791 (Translated from: GenBank U38509)
CN Protein VP1/VP2 (human parvovirus B19 strain JAP1)
CI MAN
SQL 781

SEQ 1 MSKESGKWWE SDDKFAKAVY EQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 HPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSED LHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPAKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT D KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGDPKPF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAAKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 33 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-84-6 REGISTRY
CN Protein VP1 (B19 virus strain KOR2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47793
CN GenBank AAB47793 (Translated from: GenBank U38511)
CN Protein VP1/VP2 (human parvovirus B19 strain KOR2)
CI MAN
SQL 781

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSED LHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPAKS
251 MWSEGATFTA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT D KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGDPKPF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE

09/991433

===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 34 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-83-5 REGISTRY
CN Protein VP1 (B19 virus strain KOR1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47792
CN GenBank AAB47792 (Translated from: GenBank U38510)
CN Protein VP1/VP2 (human parvovirus B19 strain KOR1)
CI MAN
SQL 781

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVQFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGEDAVL SSED LHKPGQ VSVQLPGTNY IGPNGELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYEPEHR YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQH LIENYGS IAPDALTVTI
351 SEIAVKDVT KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLG G DPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGDAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =

651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 35 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-82-4 REGISTRY
CN Protein VP1 (B19 virus strain VEN1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAA83558
CN GenBank AAA83558 (Translated from: GenBank U31358)
CN Protein VP1/VP2 (human parvovirus B19 strain VEN1)
CI MAN
SQL 781

SEQ 1 MSKESGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSED LHKPGQ VSVQLPGTNY VGPNGELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVNS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL NQH LIENYGS IAPDALTVTI
351 SEIAVKDVT KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG

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451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTOQYTD QIERPLMVGS VWNRRALHYE

=====

651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 36 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-81-3 REGISTRY
CN Protein VP1 (B19 virus strain BRZ1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47801
CN GenBank AAB47801 (Translated from: GenBank U38546)
CN Protein VP1/VP2 (human parvovirus B19 strain BRZ1)
CI MAN
SQL 781

SEQ 1 MSKESGKWE SDDKFAKAVY QQFVEFYKKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSED LHKPGQ VSVQLPGTNY VPGNELQAG PPQSAVDSAA
151 RIHDFRYSQ LAKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSPNVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FOHLIENYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTOQYTD QIERPLMVGS VWNRRALHYE

=====

651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 37 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-80-2 REGISTRY
CN Protein VP1 (B19 virus strain UK1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47794
CN GenBank AAB47794 (Translated from: GenBank U38512)
CN Protein VP1/VP2 (human parvovirus B19 strain UK1)
CI MAN
SQL 781

SEQ 1 MSKESGKWE SDNKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSSH
101 AEPRGENAVL SSED LHKPGQ VSVQLPGTNY VPGNELQAG PPQSAVDSAA
151 RIHDFRYSQ LAKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSPNVKS

09/991433

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251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLF FQHLENIYGS IAPDALVTI
351 SEIAVKDVTG KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPGL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
=====
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
```

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 38 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-79-9 REGISTRY
CN Protein VP1 (B19 virus strain USA5) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47799
CN GenBank AAB47799 (Translated from: GenBank U38517)
CN Protein VP1/VP2 (human parvovirus B19 strain USA5)
CI MAN
SQL 781

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SEQ      1 MSKESGKWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
      51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSH
     101 AEPRGENAVL SSEDLHKPGQ VSVQLPGTNY VPGNELQAG PPQSAVDSAA
     151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
     201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTS VNSAEASTGA GGGGSPVKS
     251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
     301 VCTISPIMGY STPWRYLDFN ALNLFFSPLF FQHLENIYGS IAPDALVTI
     351 SEIAVKDVTG KTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
     401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
     451 TGGTATMSYK FPLVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
     501 RSLTHEDHAI QPQNFMGPGL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
     551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
     601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
=====
     651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
     701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
     751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L
```

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 39 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-78-8 REGISTRY
CN Protein VP1 (B19 virus strain USA4) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47798
CN GenBank AAB47798 (Translated from: GenBank U38516)
CN Protein VP1/VP2 (human parvovirus B19 strain USA4)
CI MAN
SQL 781

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SEQ      1 MSKESGKWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
```

09/991433

51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSH
101 AEPRGENAVL SSDDLHKPGQ VSVQLPGTNY VGPGENELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGANFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQHLIENYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE

=====

651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPPVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 40 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 183389-77-7 REGISTRY
CN Protein VP1 (B19 virus strain USA2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB47796
CN GenBank AAB47796 (Translated from: GenBank U38514)
CN Protein VP1/VP2 (human parvovirus B19 strain USA2)
CI MAN
SQL 781

SEQ 1 MSKESGKWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHTLSSSSSH
101 AEPRGENAVL SSDDLHKPGQ VSVQLPGTNY VGPGENELQAG PPQSAVDSAA
151 RIHDFRYSQ AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGANFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQHLIENYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK FPPVPPENLE GCSQHFYEMY NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMPGPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE

=====

651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTTLVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPPVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

REFERENCE 1: 126:2046

L4 ANSWER 41 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 181380-31-4 REGISTRY
CN Protein VP (B19 virus strain Stu capsid reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein VP 1 (human parvovirus B19 strain USA1)
CN Protein VP1/VP2 (human parvovirus B19 strain USA1)

09/991433

CI MAN
SQL 781

SEQ 1 MSKESGKWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSH
101 AEPRGEDAVL SSDDLHKPGQ VSVQLPGTNY VGPGNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVVDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYPSTMS VNSAEASTGA GGGGSNPVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPL FQHLENIYGS IAPDALVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAP
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTATMSYK EPPVPPENLE GCSQHFIYEM NPLYGSRPLV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTQQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITTIVQYAV GIMTVMTTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKPEE LWTAKSRVHP L

HITS AT: 622-631

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 126:2046

REFERENCE 2: 125:213792

L4 ANSWER 42 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 167615-00-1 REGISTRY
CN Protein, VP 2 (human parvovirus clone pVP) (9CI) (CA INDEX NAME)
CI MAN
SQL 554

SEQ 1 MTSVNSAEAS TGAGGGGSGNP VKSMWSEGAT FSANSVTCTF SRQFLIPYDP
51 EHHYKVFSPA ASSCHNASGK EAKVCTISPI MGYSTPWRYL DFNALNLFFS
101 PLEFQHLENI YGSIAPDAL VTISEIAVKD VTDKTGGGVQ VTDSTTGRLC
151 MLVDHEYKYP YVLGGQDQTL APELPIWVYF PPQYAYLTVG DVNTQGISGD
201 SKKLASEESA FYVLEHSSFQ LLGTGGTATM SYKFPPVPPE NLEGCSQHFY
251 EMYNPLYGSR LGVPDTLGGD PKFRSLTHED HAIQPQNFM GPLVNSVSTK
301 EGDSSNTGAG KALTGLSTGT SQNTRISLRP GPVSQPYHHW DTDKYVTGIN
351 AISHGQTTYG NAEDKEYQQG VGRFPNEKEQ LKQLQGLNMH TYFPNKGTTQ
===== =
401 YTDQIERPLM VGSVWNRRAL HYESQLWSKI PNLDDSKTQ FAALGGWGLH
=====
451 QPPPQIFLKI LPQSGPIGGI KSMGITTIVQ YAVGIMVTM TFKLGPRKAT
501 GRWNPPQGVY PPHAAGHLPY VLYDPTAIDA QQHRRHGYEK PEELWTAKSR
551 VRPL

HITS AT: 395-404

REFERENCE 1: 123:190542

L4 ANSWER 43 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN
RN 167614-99-5 REGISTRY
CN Protein, VP 1 (human parvovirus clone pVP) (9CI) (CA INDEX NAME)
CI MAN
SQL 784

09/991433

SEQ 1 MSKESGKWWE SDDKFAKAXY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF XXLVARIKNN LKNSPDLYSH HFQSHGQLSD HPHALSSSSS
101 NAEPRGENAV LSSEDLHKPG QVSVQLPGTN YVGPGNELQA GPPQSAVDSA
151 ARIHDFRYSQ LAKLGINPYT HWTVADEELL KNIKNETGFQ AQVVKDYFTL
201 KGAAAPVAHF QGSLPEVPAY XXXASEKYPS MTSVNSAEAS TGAGGGGSSNP
251 VKSMWSEGAT FSANSVTCTF SRQFLIPYDP EHHYKVFSPA ASSCHNASGK
301 EAKVCTISPI MGYSTPWRYL DFNALNFFS PLEFQH LIEN YGSIAPDALT
351 VTISEIAVKD VTDKTGGGVQ VTDSTTGRLC MLVDHEYKYP YVLGQGQDTL
401 APELPIWVYF PPQYAYLTVG DVNTQGIGSD SKKLASEESA FYVLEHSSFQ
451 LLGTGGTATM SYKFPPVPPE NLEGCSQHFY EMYNPLYGSR LGVPDTLGGD
501 PKFRSLTHED HAIQPQNFMP GPLVNSVSTK EGDSSNTGAG KALTGLSTGT
551 SQNTRISLRP GPVSQPYHHW DTDKYVTGIN AISHGQTTYG NAEDKEYQQG
601 VGRFPNEKEQ LKQLQGLNMH TYFPNKGTTQ YTDQIERPLM VGSVWNRRA
=====
651 HYESQLWSKI PNLDDSFKTQ FAALGGWGLH QPPPQIFLKI LPQSGPIGGI
701 KSMGITTIVQ YAVGIMTVTM TFKLGPRKAT GRWNPQPGVY PPHAAGHLPY
751 VLYDPTAIDA KQHHRHGYEK PEELWTAKSR VRPL

HITS AT: 625-634

REFERENCE 1: 123:190542

L4 ANSWER 44 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN

RN 138158-34-6 REGISTRY

CN (367-686)-(707-781)-Protein VP1 (B19 virus clone pYT103 reduced),
367-L-methionine-368-L-threonine-369-L-methionine-370-L-isoleucine-
371-L-threonine-372-L-proline-373-L-serine-374-L-leucine-375-L-
histidine-376-L-alanine-377-L-cysteine-378-L-methionine-379-L-
leucine-380-L-valine- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 367-686)-(707-781)-Protein VP 1 (human parvovirus B19 clone pYT103
reduced), 367-L-methionine-368-L-threonine-369-L-methionine-370-L-
isoleucine-371-L-threonine-372-L-proline-373-L-serine-374-L-leucine-
375-L-histidine-376-L-alanine-377-L-cysteine-378-L-methionine-379-L-
leucine-380-L-valine-

CI MAN

SQL 395

SEQ 1 MTMITPSLHA CMLVDHEYKY PYVLGQGQDT LAPELPIWVY FPPQYAYLTV
51 GDVNTQGIGS DSKKLASEES AFYVLEHSSF QLLGTGGTAS MSYKFPPVPP
101 ENLEGCSQHF YEMYNPLYGS RLGVPDTLGG DPKFRSLTHE DHAIQPQNF
151 PGPLVNSVST KEGDSSNTGA GKALTGLSTG TSQNTRISLR PGPVSQPYHH
201 WDTDKYVTGI NAISHGQTTY GNAEDKEYQQ GVGRFPNEKE QLKQLQGLNM
251 HTYFPNKGTTQ QYTDQIERPL MVGSVWNRRA LHYESQLWSK IPNLDDSFKT
=====
301 QFAALGGWGL HQPPPQIFLK QYAVGIMTVT MTFKLGPRKA TGRWNPQPGV
351 YPPHAAGHLP YVLYDPTATD AKQHHRHGYE KPEELWTAKS RVHPL

HITS AT: 256-265

REFERENCE 1: 116:19653

L4 ANSWER 45 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN

RN 138158-32-4 REGISTRY

CN (219-686)-(707-781)-Protein VP1 (B19 virus clone pYT103 reduced),
219-L-methionine-220-L-threonine-221-L-methionine-222-L-isoleucine-
223-L-threonine-224-L-asparagine-225-L-serine-226-L-leucine-227-L-
isoleucine- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN (219-686)-(707-781)-Protein VP 1 (human parvovirus B19 clone pYT103

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reduced), 219-L-methionine-220-L-threonine-221-L-methionine-222-L-
isoleucine-223-L-threonine-224-L-asparagine-225-L-serine-226-L-
leucine-227-L-isoleucine-

CI MAN
SQL 543

SEQ 1 MTMITNSLIM TSVNSAEAST GAGGGGSNSV KSMWSEGATF SANSVTCTFS
51 RQFLIPYDPE HHYKVFSPAA SSCHNASGKE AKVCTISPIM GYSTPWRYLD
101 FNALNLFFSP LEFQHLENIY GSIAPDALTV TISEIAVKDV TDKTGGGVQV
151 TDSTTGRLCM LVDHEYKYPY VLGQGQDTLA PELPIWVYFP PQYAYLTVGD
201 VNTQGISGDS KKLASEESAF YVLEHSSFQ LGTGGTASMS YKFPVPVPPEN
251 LEGCSQHFEY MYNPLYGSRL GVPDTLGGDP KFRSLTHEDH AIQPQNFMGP
301 PLVNSVSTKE GDSSNTGAGK ALTGLSTGTS QNTRISLRPG FVSQPYHHWD
351 TDKYVTGINA ISHGQTTYGN AEDKEYQQGV GRFPNEKEQL KQLQGLNMHT
401 YFPNKGTTQY TDQIERPLMV GSVWNRALH YESQLWSKIP NLDDSFKTQF
===== ===
451 AALGGWGLHQ PPPQIFLKQY AVGIMTVTMT FKLGP RKATG RWNPPQGVYP
501 PHAAGHLPYV LYDPTATDAK QHHRHGYEKP EELWTA KSRV HPL

HITS AT: 404-413

REFERENCE 1: 116:19653

L4 ANSWER 46 OF 46 REGISTRY COPYRIGHT 2004 ACS on STN

RN 103351-69-5 REGISTRY

CN Protein VP1 (B19 virus clone pYT103 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Protein VP 1 (human parvovirus B19 clone pYT103 reduced)

CI MAN

SQL 781

SEQ 1 MSKKSGKWWE SDDKFAKAVY QQFVEFYEKV TGTDLLELIQI LKDHYNISLD
51 NPLENPSSLF DLVARIKNNL KNSPDLYSHH FQSHGQLSDH PHALSSSSSH
101 AEPRGENAVL SSED LHKPGQ VSVQLPGTNY VGP GNELQAG PPQSAVDSAA
151 RIHDFRYSQL AKLGINPYTH WTVADEELLK NIKNETGFQA QVVKDYFTLK
201 GAAAPVAHFQ GSLPEVPAYN ASEKYP SMTS VNSAEASTGA GGGGSNSVKS
251 MWSEGATFSA NSVTCTFSRQ FLIPYDPEHH YKVFSPAASS CHNASGKEAK
301 VCTISPIMGY STPWRYLDFN ALNLFFSPLE FQHLENIYGS IAPDALTVTI
351 SEIAVKDVT DKTGGGVQVTD STTGRLCMLV DHEYKYPYVL GQGQDTLAPE
401 LPIWVYFPPQ YAYLTVGDVN TQGISGDSKK LASEESAFYV LEHSSFQLLG
451 TGGTASMSYK FPPVPPENLE GCSQHFEYEM NPLYGSRLGV PDTLGGDPKF
501 RSLTHEDHAI QPQNFMGPPL VNSVSTKEGD SSNTGAGKAL TGLSTGTSQN
551 TRISLRPGPV SQPYHHWDTD KYVTGINAIS HGQTTYGNAE DKEYQQGVGR
601 FPNEKEQLKQ LQGLNMHTYF PNKGTTQYTD QIERPLMVGS VWNRRALHYE
===== =
651 SQLWSKIPNL DDSFKTQFAA LGGWGLHQPP PQIFLKILPQ SGPIGGIKSM
701 GITT LVQYAV GIMTVTMTFK LGPRKATGRW NPQPGVYPPH AAGHLPYVLY
751 DPTATDAKQH HRHGYEKP EE LWTAKSRVHP L

HITS AT: 622-631

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 105:55398

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